AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows.

Page 13, third full paragraph (page 13, line 21-page 14, line 3): In a most preferred embodiment of the present method, PCR is used for amplifying the subject's nucleic acids, particularly from a *PARP* region. Briefly, a thermal resistant DNA polymerase (e.g., *Taq* polymerase), and *PARP*-specific primers are employed to amplify the genomic DNA to produce *PARP* gene-specific amplification products. If PCR is used, any combination of oligonucleotide primers that will amplify nucleic acid sequences of the *PARP* region, or parts thereof, can be employed. Useful primer sequences are readily available, for example, from the GENBANK ~~GenBank~~ database (National Center for Biotechnology Information (NCBI), Bethesda, MD; www.ncbi.nlm.nih.gov/BLAST/). Most preferably, amplification of the subject's nucleic acids can be achieved using a set of oligonucleotide primers comprising a 5' (forward) primer sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID. NO.:1) or a 3' (reverse) primer sequence AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2), or a fragment of either of these at least 18 nucleotides long. But also preferred in practicing the inventive method is any other embodiment of the inventive primer set as described hereinbelow.

Page 14, second full paragraph (page 14, line 18-page 15, line 3): *PARP*-specific polynucleotides are determined by base sequence similarity or homology to (SEQ. ID. NO.:5). Base sequence homology is determined by conducting a base sequence similarity search of a genomics data base, such as the GENBANK ~~GenBank~~ database

~~of the National Center for Biotechnology Information (NCBI; www.ncbi.nlm.nih.gov/BLAST/)~~, using a computerized algorithm, such as PowerBLAST, QBLAST, PSI-BLAST, PHI-BLAST, gapped or ungapped BLAST, or the "Align" program through the Baylor College of Medicine server (www.hgsc.bcm.tmc.edu/seq_data). (E.g., Altschul~~Altchul~~, S.F., *et al.*, *Gapped BLAST and PSI-BLAST: a new generation of protein database search programs*, Nucleic Acids Research 25(17):3389-402 [1997]; Zhang, J., & Madden, T.L., *PowerBLAST: a new network BLAST application for interactive or automated sequence analysis and annotation*, Genome Res. 7(6):649-56 [1997]; Madden, T.L., *et al.*, *Applications of network BLAST server*, Methods Enzymol. 266:131-41 [1996]; Altschul, S.F., *et al.*, *Basic local alignment search tool*, J. Mol. Biol. 215(3):403-10 [1990]). Preferably, a *PARP*-specific polynucleotide sequence is at least 5 to about 30 contiguous nucleotides long, more preferably at least 6 to 15 contiguous nucleotides long, and most preferably at least 7 to 10 contiguous nucleotides long.

Page 16, second full paragraph (page 16, lines 9-19): In a most preferred embodiment of the present method that employs nucleotide sequencing, sequencing of *PARP* may be accomplished by using fluorescence-based single strand conformation polymorphism analysis (SSCP), a routine and reliable means of identifying point mutations, small insertions or deletions. (J.S. Ellison, *Fluorescence-based mutation detection. Single-strand conformation polymorphism analysis [F-SSCP], Mol. Biotechnol. 5(1):17-31 [1996]*; H. Iwahana *et al., Multiple fluorescence-based PCR-SSCP analysis using internal fluorescent labeling of PCR products*, Biotechniques

21(3):510-14, 516-19 [1996]; R. Makino *et al., F-SSCP: fluorescence-based polymerase chain reaction-single-strand conformation polymorphism [PCR-SSCP]*, PCR Methods Appl. 2(1)10-13 [1992]). An automated system may be used, such as an Applied Biosystems DNA sequencer, equipped with GENESCAN 672 (Perkin-Elmer, Applied Biosystems Division, Foster City, CA), ~~Genetyper~~ GENOTYPER (Perkin-Elmer, Applied Biosystems Division), or another appropriate analytical software package.

Page 18, first full paragraph (page 18, lines 1-8): Any of diverse fluorescent dyes are optionally used to label primers or amplification products for ease of analysis, including but not limited to, SYBR Green I (a cyclic-substituted unsymmetrical cyanine dye that emits at 519nm when excited at 494nm, Chemical Abstract Service Registry Number CAS 163795-75-3, *Chemical Abstracts, 13th Collective Chemical Substance Index* [1992-1996]) (Molecular Probes, Inc., Eugene, OR), YO-PRO-1 (quinolinium,4-[(3-methyl-2(3H)-benzoxazolylidene) methyl]-1-[3-(triemthylammonio) propyl]-, diiodide) (Molecular Probes, Inc.), thiazole orange (1,1'-(4,4,8,8-tetramethyl-4,8-diazaundecamethylene)-bis[4-[3-methyl-2,3-dihydro(benzo-1,3-thiazole)-2-methylidene]]quinolinium tetraiodide), Hex (6-carboxy-2',4'7',4,7-hexachlorofluoresceinhexachlorofluorescein), FAM (6-carboxyfluorescein), or TET (4,7,2',7'-tetrachloro-6-carboxyfluoresceincarboxyfluorescein). (E.g., J. Skeidsvoll and P.M. Ueland, *Analysis of double-stranded DNA by capillary electrophoresis with laser-induced fluorescence detection using the monomeric dye SYBR green I*, Anal. Biochem. 231(20):359-65 [1995]; H. Iwahana *et al.*, *Multiple fluorescence-based PCR-*

SSCP analysis using internal fluorescent labeling of PCR products, Biotechniques 21(30):510-14, 516-19 [1996]).

Page 23, first full paragraph (page 23, lines 3-18): To determine genotypes of *PARP*, we used the 5' oligonucleotide primer sequence 5'-GAT TCC CCA TCT CTC TTT CTT T-3' (SEQ. ID. NO.:1) tagged with the fluorescent dye 6FAM and the 3' oligonucleotide primer sequence 5'-AAA TTG TGG TAA TGA CTG CA-3' (SEQ. ID. NO.:2). The PCR condition for this polymorphism was 30 cycles of 93°C for 1 min, 56°C for 30 s, and 72°C for 1 min plus a final extension of 72°C for 5 min. For the intronic dinucleotide repeat of *HLXI*, the 5' oligonucleotide primer sequence was 5'-TTC ACA CAA GTT CCA GCT TCC CTT-3' (SEQ. ID. NO.:3) tagged with the fluorescent dye TET, and the 3' oligonucleotide primer sequence was 5'-TGC TGT CTC TGT TTC TTT CTG ACC-3' (SEQ. ID. NO.:4). The *HLXI* PCR condition was 10 cycles~~cyles~~ of 94°C for 15 s, 55°C for 15 s, and 72°C for 30 s, then followed by 20 cycles of 89°C for 15 s, 55°C for 15 s and 72°C for 30 s with a final extension at 72°C for 10 min. For these two candidate genes, PCR mixture contained 40 ng genomic DNA, 20 mM Tris-HCl[[L]] pH8.0, 2 mM $MgCl_2$, 10 mM KCl, 6 mM $(NH_4)_2SO_4$, 0.1% Triton X-100, 10 μg/ml BSA, 0.5 Units of native *Pfu* DNA polymerase (Stratagene, San Diego, CA), 200 μM dNTP, and 0.2 μM primers in 5 μl reaction. Aliquots of fluorescent PCR products were electrophoresed using a 377 ABI PRISM ~~Prism ABI~~ sequencer (Perkin-Elmer, Applied Biosystems Division~~, Foster City, CA~~) and analyzed by GENESCAN ~~GeneScan~~ and GENOTYPER ~~Genotyper~~ programs.